

Practitioner's Docket No. MPI01-019P1RNM

PATENT

In re application of:	Olandt, Peter J. et al.		
Application No.:	10/074,527	Group No.:	1652
Filed:	February 12, 2002	Examiner:	Rao, Manjunath N.
For:	33945, A HUMAN GLYCOSYLTRANSFERASE AND USES THEREFOR		

Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

DECLARATION UNDER 37 C.F.R. § 1.131

Sir:

We, Peter J. Olandt, Rachel E. Meyers, and Katherine M. Galvin hereby declare and state:

1. In the United States, the conception of the sequence of the human 33945 molecules of the invention and the identification of the 33945 polypeptide as a glycosyltransferase occurred prior to December 15, 2000 and the reduction to practice comprising obtaining the final sequence known as SEQ ID NO:1 in the above-identified application was performed with due diligence until December 18, 2000, the date of the actual reduction to practice.
2. Evidence of conception prior to December 15, 2000 is provided in Exhibits A1-A3, which are copies of electronic printouts of a map of clones contributing to the 33945 nucleotide sequence and analyses of early 33945 sequences.

Exhibit A1 is a copy of page 1 of a Sequencher™ map identifying the clones contributing to the 33945 nucleotide sequence, the clone sizes and the positions of the clones relative to the 33945 sequence known at that stage of the invention process. Exhibit A2 is a copy of a BLAST analysis of a translation of that nucleotide sequence. The map was compiled and the analysis was

CERTIFICATION UNDER 37 C.F.R. SECTIONS 1.8(a) and 1.10*

I hereby certify that, on the date shown below, this correspondence is being:

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37 C.F.R. SECTION 1.8(a)

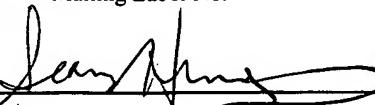
37 C.F.R. SECTION 1.10*

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Signature
Sean Hunziker/Beverly Sotiropoulos

Date: August 9, 2004

(type or print name of person certifying)

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performed prior to December 15, 2000. By that time, the sequence was extensive, spanning 2109 nucleotides, and the BLAST revealed similarity of the 33945 polypeptide to glycosyltransferases. Exhibit A3 is a copy of a series of analyses performed on the polypeptide encoded by that 33945 nucleotide sequence. Page 1 of this printout bears the nearly complete polypeptide sequence known at the time, showing that it has the full length of 581 amino acids, but a few uncertain residues; page 3 bears the results of a Pfam analysis which matched a portion of the 33945 sequence with the Pfam Glycosyl transferase domain consensus sequence; pages 4 and 5 bear the results of an analysis which matched portions of the 33945 polypeptide sequence with glycosyltransferase domain consensus sequences from the ProDom database. The combined result of the analyses was the determination that the 33945 molecules of the invention represent a glycosyltransferase.

The original printouts in Exhibits A1-A3 bear the automatically embedded dates on which the analyses were performed. In accordance with accepted practice, the dates on the copies of the electronic printouts have been masked (M.P.E.P. § 715.07).

3. Evidence of the exercise of due diligence in the process of reducing to practice the 33945 molecules of the invention is provided in Exhibits B1-B5. In accordance with M.P.E.P. § 715.07, the actual dates of the acts portrayed in Exhibits B1-B5 have been provided to establish diligence. In accordance with M.P.E.P. § 715.07(a), the acts performed just prior to the effective date of December 15, 2000 until the December 18, 2000 date of the actual reduction to practice are included in Exhibits B1-B5.

Exhibit B1 is a copy of page 1 of an updated Sequencher™ map compiling the clones contributing to the 33945 nucleotide sequence as understood by November 27, 2000. One can see from this Exhibit, additional 5' clones "fbhX33945phg01b1.abi" and "fbhX33945phh01b1.abi" which were not present on Exhibit A1. In addition, Exhibit B1 has a note written by inventor Peter Olandt, describing a 2 base pair problem needing to be solved. In order to solve this problem, additional clones were prepared to cover the region in question. This clone preparation process yielded four additional 5' clones, "fbhX33945peb04h1," "fbhX33945pee03g1," "fbhX33945pf04h1" and "fbhX33945pfg03g1."

Clone fbhX33945pee03g1 is used herein as an example of the timecourse and types of analyses performed on these clones to show due diligence. Exhibit B2 provides a summary of the facts related to clone fbhX33945pee03g1, together with its nucleotide sequence. At the top of Exhibit B2, one can see that this clone was submitted for sequencing on December 12, 2000. As seen in the middle of the Exhibit, fbhX33945pee03g1 came out of sequencing on December 14, 2000 and was submitted for analyses. The first analysis was performed on December 14, 2000, and subsequent analyses were performed on December 15 and 16, 2000.

Exhibit B3 shows that on Monday, December 18, 2000, the four new clones were assembled into a new Sequencher™ clone map. The problem of base pair selection was solved and the complete 33945 nucleic acid sequence ("Fbh33945FL"), known in the application as SEQ ID NO:1 was finalized and submitted to the Millennium database on Monday, December 18, 2000, as shown on Exhibit B4. Exhibit B5, also performed on December 18, 2000, shows that analyses performed on the polypeptide encoded by the complete nucleotide sequence supported the earlier conclusion of 33945 as a glycosyltransferase drawn from the evidence of prior conception provided in Exhibits A2 and A3.

We hereby declare that all statements made herein of our own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or

imprisonment, or both, under Section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

Peter J. Olandt

Date

Rachel E. Meyers

Date

Katherine Galvin
Katherine M. Galvin

7-16-04
Date

**Exhibit A1 to Accompany Declaration under
37 CFR §1.131 for US Appln. No. 10/074,527**

33945
Sequencher™ "33945"

fbhX33945pgbb02b1.abi, 1 to 371
 fbhX33945pgba01a1.abi, 1 to 373
 fbhX33945pgba02b1.abi, 1 to 380
 fbhX33945pgbb01a1.abi, 13 to 373
 AL136084.nt|GENSCAN_predicted_C, 221 to 569
 AI863865 in DBEst, 226 to 727
 AA493187 in DBEst, 261 to 593
 AA429394 in DBEst, 265 to 727
 AI800923 in DBEst, 269 to 822
 AA807096 in DBEst, 334 to 574
 AA836046 in DBEst, 518 to 737
 AL136084.nt|GENSCAN_predicted_C, 570 to 760
 AA401053 in DBEst, 620 to 1096
 AA429393 in DBEst, 623 to 1096
 AL136084.nt|GENSCAN_predicted_C, 758 to 1241
 BE167242 in DBEst, 962 to 1138
 AW843782 in DBEst - Import - c, 1104 to 1329
 AW814059 in DBEst - Import - c, 1175 to 1395
 johnh204g03t1.abi, 1197 to 1591
 jthAa158a12t1.abi, 1203 to 1600
 AL136084.nt|GENSCAN_predicted_C, 1241 to 1774
 jThzc1157a07t1.abi, 1257 to 1425
 chbne001h07j0t1.abi, 1308 to 1552
 johne001h07t1.abi, 1308 to 1803
 AC007800.nt|GENSCAN_predicted_C, 1371 to 1774
 cMhqad053c04a1.abi, 1495 to 1916
 cMhvf090g07a1.abi, 1600 to 1957
 AI638649 in DBEst - Import - c, 1608 to 2063
 AA554045 in DBEst - Import - c, 1633 to 2067
 AI916034 in DBEst - Import - c, 1664 to 2067
 jihbaa033c02t1.abi, 1667 to 2067
 johnd068h12t1.abi, 1701 to 2031
 AI636959 in DBEst - Import - c, 1701 to 2076
 AA994913 in DBEst - Import - c, 1706 to 2063
 cohvBA001e10a1.abi, 1801 to 1957

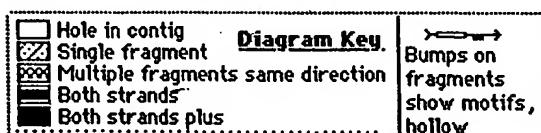
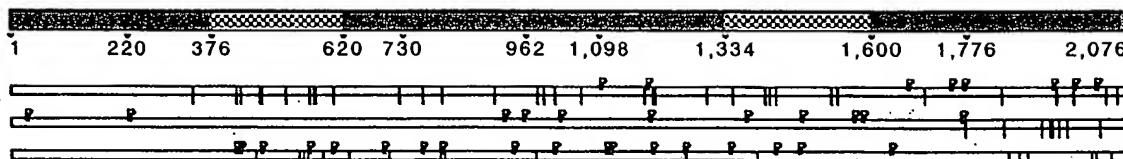


Exhibit A2 to Accompany Declaration under
37 CFR §1.131 for US Appln. No. 10/074,527

33945 (analysis only) (2109 bases) -

WU2 BLAST vs. PROT - Selected Database Hits

>gi|2121220|gb|AAB58301| (U73819) polypeptide GalNAc transferase-T4 [Mus
musculus]
Length = 578

Plus Strand HSPs:

Score = 1654 (587.3 bits), Expect = 3.7e-169, P = 3.7e-169
Identities = 328/570 (57%), Positives = 405/570 (71%), Frame = +2

Query: 128 VLLALLALAGL----GSVLRARQGAGAGAAEPGPRTPRPGRRE----PVMPRPVPA 277
+LLALL LA + S L A GAG GA E GP R P RE P+ +PP +
Sbjct: 13 LLLALLTLAYILVEFSVSTLYASPGAG-GARELGPRRLPDLDTREEDLSQPLYIKPPADS 71

Query: 278 NALGARGEAVRLQLQGEELRLQEEESVRLHQINIYLSDRISLHRRLPXRWNPLCKEKKYDY 457
+ALG G A +LQL EL+ QEE + + INIYLSDRISLHR + + CK KK+ Y
Sbjct: 72 HALGEWGRASKLQLNEGELKQQEELIERYAINIYLSDRISLHHRHIEDKRMYECKAKKFHY 131

Query: 458 DNLPRTSVIIAFYNEAWSTLLRTVSVLETSPDILLEEVILVDDYSDREHLKERLANELS 637
+LP TSVIIAFYNEAWSTLLRT++SVLETSP +LL+E+ILVDD SDR +LK +L +S
Sbjct: 132 RSLPTTSVIIAFYNEAWSTLLRTIHSVLETSPAVLLKEIILVDDLSRIYLKAQLETYIS 191

Query: 638 GLPKVRLIRANKREGLVRARLLGASAARGDVLTFLDCHECCEHGWLPEPLLQRIHEEESAV 817
L +VRLIR NKREGLVRARL+GA+ A GDVLTFLDCHEC+ GWLEPLL+RI +E+A+
Sbjct: 192 NLERVRLIRTNKREGLVRARLIGATFATGDVLTFLDCHECNGWLEPLLERISRDETAI 251

Query: 818 VCPVIDVIDWNTFEYLGNSGEPIGGFDWRLVFTWHTVPERERIRMQSPVDVIRSPTMAG 997
VCPVID IDWNTFE+ +GEP IGGFDWRL F WH+VP+ ER R S +D IRSPTMAG
Sbjct: 252 VCPVIDTIDWNTFEFYMQTGEPMIGGFDWRLTFQWHSPKHERDRRTSRIDPIRSPTMAG 311

Query: 998 GLFAVSKKYFEYLGSYDTGMEVWGENLEFSFRIWQCGVLETHPCSHVGHFRKQAPYS 1177
GLFAVSKKYF+YLG+YDTGMEVWGENLE SFR+WQCGG LE HPCSHVGHVF K+APY+
Sbjct: 312 GLFAVSKKYFQYLGTYDTGMEVWGENLELSFRVWQCGKLEIHPCSHVGHFPKRAPYA 371

Query: 1178 RNKALANSVXAAEVWMDEFKELYHRNPRARLEPFGDVTERKQLRDKLQCKDFKWLET 1357
R L N+ AAEVWMDE+KE +Y+RNP AR E +GD++ERK LR++L+CK F W+L+ V
Sbjct: 372 RPNFLQNTARAAEVWMDEYKEHFYNRNPPARKEAYGDLSERRLKCKSFDWYLKNV 431

Query: 1358 YPELHVPEDRPGFFGMLQNKGTDYCFDYNPPDENQIVGHQVILYLCMGQNFSEYTS 1537
+ LHVPEDRPG+ G +++ G++ C DYN PD N G + L+ CHG G NQFFEYTS
Sbjct: 432 FSNLHVPEDRPGWHGAIRSMGSISSCLDYNAPDNNP-TGANLSLFGCHQGGNQFFEYTS 490

Query: 1538 QKEIRYNTHQPEGCIAVEAGMDTLIMHLCEETA---PENQKFILQEDGSLFHEQSKKCVQ 1708
KEIR+N+ E C V D + M C + P N + +EDG++FH ++ C+
Sbjct: 491 NKEIRFNS-VTELCAEVPPQQKDYVGMQNCPKDGLPVPVNIIWHFKEDGTIFHPHTRLCLS 549

Query: 1709 AARKESSDSFVPLLRLDCTNSD-HQKWFFKE 1795
A R V + + C D +Q W F++
Sbjct: 550 AYRTAEGRPSVHM-KTCDALDKNQLWRFEK 578

>gi|1934912|emb|CAA69875| (Y08564) UDP-GalNAc:polypeptide
N-acetylgalactosaminyltransferase [Homo sapiens]
Length = 578

Plus Strand HSPs:

Score = 1617 (574.3 bits), Expect = 3.0e-165, P = 3.0e-165
Identities = 322/570 (56%), Positives = 399/570 (70%), Frame = +2

Query: 128 VLLALLALAG----LGSVLRAQRGAGAGAAEPGPPRTPRPGRR----EPVMPPRPPVPA 277
+LLA L +A L S A GAG A E G R + P+ +PP +
Sbjct: 13 LLLAFLTVAYIFVELLVSTFHASAGAGR-ARELGSRRLSDLQKNTEDLSPRLYKKPPADS 71

Query: 278 NALGARGEAVRLQLQGEELRLQEEESVRLHQINIYLSDRISLHRRRLPXWNPLCKEKKYDY 457
ALG G+A +LQL +EL+ QEE + + INIYLSDRISLHR + + CK +K++Y
Sbjct: 72 RALGEWGKASKLQLNEDELKQQEELIERYAINIYLSDRISLHRHIEDKRMYECKSQKFNY 131

Query: 458 DNLPRTSVIIAFYNEAWSTLLRTVYSVLETSPDILLEEVILVDDYSDRHLKERLANELS 637
LP TSVIIAFYNEAWSTLLRT++SVLETSP +LL+E+ILVDD SDR +LK +L +S
Sbjct: 132 RTLPTTSVIIAFYNEAWSTLLRTIHSVLETSPAVLLKEIILVDDLSDRVYLKTQLEYIS 191

Query: 638 GLPKVRLIRANKREGLVRARLLGASAARGDVLTFLCHCECHEGWLEPLLQRIHEEESAV 817
L +VRLIR NKREGLVRARL+GA+ A GDVLTFL CHCEC+ GWLEPLL+RI E+AV
Sbjct: 192 NLDRVRLIRTNKREGLVRARLIGATFATGDVLTFLYCHCECNSGWLEPLLERIGRYETAV 251

Query: 818 VCPVIDVIDDWNTFEYLGNSGEPQIGGFDWRLVFTWHTVPERERIRMQSPVDVIRSPTMAG 997
VCPVID IDWNTFE+ GEP IGGFDWRL F WH+VP++ER R S +D IRSPTMAG
Sbjct: 252 VCPVIDTIDWNTFEFYMQIGEPMIGGFDWRLTFQWHSVPQERDRRISRIDPIRSPTMAG 311

Query: 998 GLFAVSKKYFEYLGSYDTGMEVWGENLEFSFRIWQCGGVLETHPCSHVGHVFRKQAPYS 1177
GLFAVSKKYF+YLG+YDTGMEVWGENLE SFR+WQCGG LE HPCSHVGHVF K+APY+
Sbjct: 312 GLFAVSKKYFQYLGTYDTGMEVWGENLELSFRVWQCGGKLEIHPCSHVGHVF PKRAPYA 371

Query: 1178 RNKALANSVXAAEVWMDEFKELYHRNPRARLEPFGDVTERKQLRDKLQCKDFKWFLETV 1357
R L N+ AAEVWMDE+KE +Y+RNP AR E +GD++ERK LR++L+CK F W+L+ V
Sbjct: 372 RPNFLQNTARAAEVWMDEYKEHFYNRNP PARKEAYGDISERKLLRERLRCKSFDWYLKNV 431

Query: 1358 YPELHVPEDRPGFFGMLQNKGLTDYCFDYNPPDENQIVGHQVILYLCMGQNFSEYTS 1537
+P LHVPEDRPG+ G +++++G++ C DYN PD N G + L+ CHG G NQFFEYTS
Sbjct: 432 FPNLHVPEDRPGWHGAIERSRGISSECLDYNSPDNNP-TGANLSLFGCHGQGGNQFFEYTS 490

Query: 1538 QKEIRYNTHQPEGCIAVEAGMDTLIMHLCEETA---PENQKFilQEDGSLFHEQSKKCVQ 1708

KEIR+N+ E C V + + M C + P N + +EDG++FH S C+
Sbjct: 491 NKEIRFNS-VTELCAEVPEQKNYVGMQNCPKDGFPVPANIIWHFKEDGTIFPHSGLCLS 549

Query: 1709 AARKESSDSFVPLLRCNTSD-HQKWFFKE 1795

A R V + R C D +Q W F++

Sbjct: 550 AYRTPEGRPDVQM-RTCDALDKNQIWSFEK 578

>gi|10437274|dbj|BAB15027| (AK024865) unnamed protein product [Homo sapiens]
Length = 284

Plus Strand HSPs:

Score = 1547 (549.6 bits), Expect = 8.0e-158, P = 8.0e-158

Identities = 282/284 (99%), Positives = 282/284 (99%), Frame = +2

Query: 953 MQSPVDVIRSPTMAGGLFAVSKYFEYLGSYDTGMEVWGGENLEFSFRIWQCGGVLETHP 1132
MQSPVDVIRSPTMAGGLFAVSKYFEYLGSYDTGMEVWGGENLEFSFRIWQCGGVLETHP

Sbjct: 1 MQSPVDVIRSPTMAGGLFAVSKYFEYLGSYDTGMEVWGGENLEFSFRIWQCGGVLETHP 60

Query: 1133 CSHVGHVFRKQAPYSRNKALANSVAAEVWMDEFKELYYHRNPRARLEPGDVTTERKQLR 1312
CSHVGVHF KQAPYSRNKALANSV AAEVWMDEFKELYYHRNPRARLEPGDVTTERKQLR

Sbjct: 61 CSHVGVFPKQAPYSRNKALANSVRAAEVWMDEFKELYYHRNPRARLEPGDVTTERKQLR 120

Query: 1313 DKLQCKDFKWFLETVYPELHVPEDRPGFFGMLQNKGLTDYCFDYNPPDENQIVGHQVILY 1492
DKLQCKDFKWFLETVYPELHVPEDRPGFFGMLQNKGLTDYCFDYNPPDENQIVGHQVILY

Sbjct: 121 DKLQCKDFKWFLETVYPELHVPEDRPGFFGMLQNKGLTDYCFDYNPPDENQIVGHQVILY 180

Query: 1493 LCHGMGQNQFFEYTSQKEIRYNTHQPEGCIAVEAGMDTLIMHLCEETAPENQKFILQEDG 1672
LCHGMGQNQFFEYTSQKEIRYNTHQPEGCIAVEAGMDTLIMHLCEETAPENQKFILQEDG

Sbjct: 181 LCHGMGQNQFFEYTSQKEIRYNTHQPEGCIAVEAGMDTLIMHLCEETAPENQKFILQEDG 240

Query: 1673 SLFHEQSKKCVQAARKESSDSFVPLLRCNTSDHQKWFFKERML 1804

SLFHEQSKKCVQAARKESSDSFVPLLRCNTSDHQKWFFKERML

Sbjct: 241 SLFHEQSKKCVQAARKESSDSFVPLLRCNTSDHQKWFFKERML 284

>gi|5834600|emb|CAA69876| (Y08565) UDP-GalNAc:polypeptide

N-acetylgalactosaminyltransferase [Homo sapiens]

Length = 622

Plus Strand HSPs:

Score = 40 (19.1 bits), Expect = 9.9e-120, Sum P(2) = 9.9e-120

Identities = 8/14 (57%), Positives = 9/14 (64%), Frame = +3

Query: 204 PSRDPRAPRAPGGA 245

P +DP AP A G A

Sbjct: 106 PPQDPNAPGADGKA 119

Score = 1168 (416.2 bits), Expect = 9.9e-120, Sum P(2) = 9.9e-120
Identities = 246/537 (45%), Positives = 338/537 (62%), Frame = +2

Query: 233 PGRREPVMRPPV PANALGARGEAV-R LQLQGEELRLQEEVRLHQINIYLSDRISLHRR 409
P +P RPP NA GA G+A + + E + +EE + H N + SDRISL R
Sbjct: 96 PAELKPFWERPPQDPNAPGADGKAFQSKWTPLETQEKEEGYKKHCFNAFASDRISLQRS 155

Query: 410 L-PXRWNPLCKEKKYDY-DNLRTSVIIAFYNEAWSTLLRTVYSVLETS PDILLEEVILV 583
L P P C ++K+ L TSVII F+NEAWSTLLRTVYSVL T+P ILL+E+ILV
Sbjct: 156 LGPDTRPPECVDQKFRRCPPLATT SVIIVFHNEAWSTLLRTVYSVLHTTPAILLKEIILV 215

Query: 584 DDYSDREHLKERLANELSGLPKVRLIRANKREGLVRARLLGASAARGDVLTFLDCHECH 763
DD S EHLKE+L + L VR++R +R+GL+ ARLLGAS A+ +VLTFLD HCEC
Sbjct: 216 DDASTEEHLKEKLEQYVKQLQVVRVVRQEERKGLITARLLGASVAQAELTFLDAHCECF 275

Query: 764 EGWLEPLLQRIHEEEESAVVCPVIDVIDDWNTFEYLGSNSGEPQI---GGFDWRLVFTWHTVP 934
GWLEPLL RI E+++ VV P I ID NTFE+ ++ G FDW L F W T+P
Sbjct: 276 HGWLEPLLARIAEDKTVVSPDIVTIDLNTFEAKPVQRGRVHSRGNFDWSLTFGWETLP 335

Query: 935 ERERIRMQSPVDTVIRSPTMAGGLFAVSKKYFEYLGSYDTGMEVWGGENLEFSFRIWQCGG 1114
E+ R + I+SPT AGGLF++ K YFE++G+YD ME+WGGEN+E SFR+WQCGG
Sbjct: 336 PHEKQRKDETYPPIKSPTFAGGLFSIPKSYFEHIGTYDNQMEIWGGENVEMSFRVWQCGG 395

Query: 1115 VLETHPCSHVGHVFRKQAPYSRNKALA---NSVXAAEVWMDEFKELYHHRNPRA---R 1270
LE PCS VGHVFR ++P++ K + N V AEVWMD +K+++Y RN +A +
Sbjct: 396 QLEIIPCSVVGHVFRTKSPHTFPKGTSVIARNQVRLAEVWMDSYKKIFYRRNLQAAKMAQ 455

Query: 1271 LEFGDVTTERKQLRDKLQCKDFKWLETVYPELHVPE DRPGFFGMLQNKG LTDYCFDYNP 1450
+ FGD++ER QLR++L C +F W+L VYPE+ VP+ P F+G ++N G T+ C D
Sbjct: 456 EKSGFDISERLQLREQLHCHNF SWYLHNVPEMFV PDL TPTFYGAIKNLG-TNQCLDVG- 513

Query: 1451 PDENQIVGHQVILYLC HGMGQNQFFEYTSQKEIRYNTHQPEGCIAVEAGMDTL-IMHLCE 1627
EN G +I+Y CHG+G NQ+FEYT+Q+++R+N + +C+ V G L H
Sbjct: 514 --ENNRGGKPLIMYSCHGLGGNQYFEYTTQRDLRHNIAK-QLCLHVS KGALGLGSCHFTG 570

Query: 1628 ETA--PENQKFILQEDGSLFHEQS KKCVQAARKESSDSFVPL RDCTNSD-HQKWFF 1789
+ + P+++++ L +D + + S C+ + K+ P + C SD HQ W F
Sbjct: 571 KNSQVPKDEEWELAQDQLIRNSGSGTCLTSQDKK-----PAMAPCNPSDPHQLWLF 621

>gi|3047191|gb|AAC13671| (AF031835) GLY5a; ppGANTase [Caenorhabditis elegans]
>pir|T42245|T42245 probable polypeptide
N-acetylgalactosaminyltransferase (EC 2.4.1.41) - Caenorhabditis
elegans
Length = 623

Plus Strand HSPs:

Score = 1185 (422.2 bits), Expect = 1.8e-119, P = 1.8e-119
Identities = 252/530 (47%), Positives = 326/530 (61%), Frame = +2

Query: 251 VMPRPPV---PANALGARGEAV---RLQLQGEELRLQEESVRLHQINIYLSDRISLHRR 409
V P . P+ A G G+AV + +L EE ++ + + N Y SD IS+HR
Sbjct: 97 VDPNDPIYKKGDAAQAGELGKAVVVDKTKLSTEEKAKYDKGMLNNAFNQYASDMISVHRT 156

Query: 410 LPXRWNPLCKEKKYDYDNLPRTSVIIAFYNEAWSTLLRTVSVLESPDILLEEVLVDD 589
LP + CK +KY+ +NLPRTSVII F+NEAWS LLRTV+SVLE +PD LLEEV+LVDD
Sbjct: 157 LPTNIDAECKTEKYN-ENLPRTSVIICFHNEAWSVLLRTVHSVLERTPDHLLEEVVLVDD 215

Query: 590 YSDREHLKERLANELSGLP-KVRLIRANKREGLVVRARLLGASAARGDVLTFLDCHEC 766
+SD +H K L +S KV+++R KREGL+RARL GA+ A G+VLT+LD HCEC E
Sbjct: 216 FSDMDHTKRPLEEYMSQFGGVKILRMKEGLIRARLRGAAVATGEVLTYLDSHCECME 275

Query: 767 GWLEPLLQRIHEEESAVVCVIDVIDDWNTFEYLGNNGE-PQIGGFDWRLVFTWHTVPERE 943
GW+EPLL RI + + VVCPVIDVID NTFEY + +GGFDW L F WH++PER+
Sbjct: 276 GWMEPLLDRIKRDPTTVVCPVIDVIDDNTFEYHHSKAYFTSVGGFDWGLQFNWHISPERD 335

Query: 944 RIRMQSPVDVIRSPTMAGGLFAVSKKYFEYLGSYDTGMEVWGGENLEFSFRIWQCGGVLE 1123
R P+D +RSPTMAGGLF++ K+YFE LG+YD G ++WGGENLE SF+IW CGG LE
Sbjct: 336 RKNRTRPIDPVRSPSTMAGGLFSIDKEYFEKLGYDPGFDIWGGENLELSFKIWMCGGTLE 395

Query: 1124 THPCSHVGHVFRKQAPYS-R---NKALANSVXAAEVWMDEFKELYHRNPRARLEPGDV 1291
PCSHVGHVFRK++PY R N NS+ AEVW+D++K YY R +L FGD+
Sbjct: 396 IVPCSHVGHVFRKRSPTYKWRGVNVLRNSIRLAEVWLDDYKTYYERINN-QLGDFGDI 454

Query: 1292 TERKQLRDKLQCKDFKWLETVYPELHVPEDRPGFFGMLQNKGTDYCFDYNPPDENQIV 1471
+ RK+LR+ L CK FKW+L+ +YPEL VP + M G C DY P
Sbjct: 455 SSRKKLREDLGCKSFKWYLDNIYPELFVPGESVAKGEMRNAGGKNRQCIDYKPSG---- 509

Query: 1472 GHQVILYLCHGMGQNQFFEYTSQKEIRYNTHQPEGCIAVEAGMDTLIMHLCEETAPENQK 1651
G V +Y CH G NQ++ + EIR + E C+ AG D ++ C NQ+
Sbjct: 510 GKTVGMYQCHNQGGNQYWMLSNDGEIR---RDESCVDY-AGSDVMVFP-CHGMKG-NQE 562

Query: 1652 FILQED-GSLFHEQSCKCVQAARKESSDSFVPLLRDCTNSD-HQKWFFKE 1795
+ D G L H S+KC+ + + V C D +Q W FKE
Sbjct: 563 WRYNHDTGRLQHAVSQKCLGMTKDGALEMVA---CQYDDPYQHWKFKE 608